Figure 1A

<b>3</b> 1	agaqaqcaqctcccttcccctcqqcqaqqaqqaaqqaaqaaqaaqccaqaqaqaq	
6i	agagateateqeagetteteeteegaeeatttgaetgegaetgtgattacaaeaeegt	
121	tgatoctacgaaaaagaggtaatggatactggcggcaattcgctggcgtccggacctgat M D T G G N S L A S G P D	1.3
1.80	gqtqtgaagaggaaagtttqttatttctatgaccctgaggtcggcaattactactatggc	
	G V K R K V C Y F Y D P E V G N Y Y Y G	3.3
241	caaqqteateccatgaagccccateqeatecgcatgacccatqccctccteqetcactac	
	OGHPMKPHRIRMTHALLAHY	53
301	ggteteetteageatatgeaggtteteaageeetteeétgeeegggaacgtgatetetge G L L Q H M Q V L K P F P A R E R D L C	7.3
361	egettecaegeegaetatgietettiteteegeageattaceeetgaaaeceageaa	
	R F H A D D Y V S F L R S I T P E T Q Q	93
421	gatcagattcgccaacttaagcgcttcaatgttgqtgaagactgtcccgtctttgacggc	117
	DQIRQLKRFNVGEDCPVFDG	113
481	ctttattccttttgccagacctatgctggaggatctgttggtggctctgtcaagcttaac L Y S F C Q T Y A G G S V G G S V K L N	133
541	cacggcctctgcgatattgccatcaactgggctggtggtctccatcacgctaagaagtgc	
	H G L C D I A I N W A G G L H H A K K C	153
601	gaggeetetggetetgttaegteaatgatategtettagetateetagageteettaag	173
	E A S G F C Y V N D I V L A I L E L L K cagcatgagcqtgttctttatgtcgatattgatatccaccacggggatggagtggaggag	1/5
66 L	OHERVEY DIDIHEGO GVEE	193
721	gcattttatgctactgacagggttatgactgtcfcgtttcataaatttggtgattacttt	
	A F Y A T D R V M T V S F H K F G D Y F	213
781	eccygtacaggtcacattcaggatataggttatggtagcggaaagtactattctctcaat	233
0.43	The state of the s	200
841	V P L D D G I D D E S Y H L L F K P I M	25.3
901	gggaaagttatggaaattttccgaccaggggctgtggtattgcaatgtggtgctgactcc	
	G K V M E I F R F G A V V L Q C G A D S	273
961	ctatctggggatcggttaggttgcttcaatctttcaatcaa	293
1021	L S G D R L G C F N L S I K G H A B C V aaatttatgagatcgttcaatgttcccctactgctcttgggtggttggt	220
	K F M R S F N V P L L L G G G G Y T I	313
1081	cgcaatgttgcccgttgctggtgctacgagactggagttgcacttggagttgaagttgaa	205
	R N V A R C W C Y E T G V A L G V E V E	333
1141	gacaagatgccggagcatgaatattatgaatactttggtccagactatacacttcacgtt D K M P E H E Y Y E Y F G P D Y T L H V	353
1201	gctccaagtaacatggaaaataagaattctcgtcagatgcttgaagagattcgcaatgac	
	APSNMENKNSRQMLEEIRND	373
1261	ctfctccacaatctctctaagcttcagcatgctccaagtgtaccatttcaggaaagacca	393
1 201	L L H N L S K L Q H A P S V P F Q E R P cotgatacagagactcccgaggttgatgaagaccaagaagatggggataaaagatgggat	232
1321	PDTETPEVDEDQEDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	413
1381	ccggattcagacatggatgttgatgatgaccgfaaacctataccaagcagagtaaaaaga	
	PDSDMDVDDDRKPLPSRVKR	433
1441	gaagotgttgaaccaqatacaaaggacaaggactgaaaggaattatggaqcgtgga	453
1 5 0 1	E A V E P D T K D K D G L K G I M E R G aaaggttgtgaggtggaggtgaagcactaaggttacaggagtaaaccca	400
F-30/T	K G C E V E V D E S G S T K V T G V N P	473
1561	gtgggagtggaggaagcaagtgtgaaaatqgaagaggaagqaacaaacaaqggtggggcg	
	V G V E E A S V K M E E E G T N K G G A	4.93
1621	qaqcaqqcqtttcctcctaaaacataaqactcqqaqcttctaatttcttqctactttttc	501
1 (10) 1	E Q A F P P K T * tigtid abrabatigt tight about the tigtig tight ababication of the	N/ L
$\frac{1501}{1741}$	ththagaggatigaggaraga) atgratthathodfighatutofgatatgatatgat	
	atiganaa	

### Figure 1B

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$\frac{1}{2}$	gtgcccacaactcctagtaatgactttctcaggcattgttgacacaaattttgctctgagtaaaacttgggaatagagagag	
61 `ما	taaaacttgggaatagagagactctgagtgagagagaccctgagtgag	
	atggaggcagacgaaagcggcatctctctgccgtcgggacccgacggacg	20
181	gtcagttacttctacgagccgacgatcggagactactactacggtcaaggccacccgatg V S Y F Y E P T I G D Y Y Y G Q G H P M	40
241	aagcetcaceggateegtatggeteatageetaateatteaetateaeeteeaeegtege K P H R I R M A H S L I I H Y H L H R R	60
301	ttagaaatcagtcgcctagcctcgctgacgcctccgatatcggccgattccattcgccg	8.0
361	gagtatgttgacttcctcgcttccgtttcgccggaatctatgggcgatccttccgctgca	
421	E Y V D F L A S V S P E S M G D P S A A cgaaacctaaggcgattcaatgtcggtgaggattgtcctgtcttcgacggactttttgat	100
	RNLRRFNVGEDCPVFDGLFD	120
	ttttgccgtgcttccgccggaggttctattggtgctgccgtcaaattaaacagacag	140
541	gctgatatcgctatcaattggggcggtgggcttcaccatgctaagaaaagcgaggcttct A D I A I N W G G G L H H A K K S E A S	160
601	gggttttgctatgtaaacgacatcgtgctagggattctggagttgctcaagatgtttaag	180
661	cgggttctctacatagatattgatgtccaccatggagatggagtggaagaagcgttttac	
721	R V L Y I D I D V H H G D G V E E A F Y accactgatagagttatgactgtttctttccacaaatttggggactttttccaggaact	200
	T T D R V M T V S F H K F G D F F P G T ggtcacataagagatgttggcgctgaaaaagggaaatactatgctctaaatgttccacta	220
	G H I R D V G A E K G K Y Y A L N V P L	240
	<pre>aacgatggtatggacgatgaaagtttccgcagcttgtttagacctcttatccagaaggtt N D G M D D E S F R S L F R P L I Q K V</pre>	260
	atggaagtgtatcagccagaggcagttgttcttcagtgtggtgctgactccttaagtggt M E V Y Q P E A V V L Q C G A D S L S G	280
961	gatcggttgggttgcttcaacttatcagtcaagggtcacgctgattgccttcggttctta D R L G C F N L S V K G H A D C L R F L	300
1021	agatettacaacgtteeteteatggtgttgggtggatgggtgataetattegaaatgtt R S Y N V P L M V L G G E G Y T I R N V	320
1081	gccgttgctggtgttatgagactgcagttgctgttggagtagagccggacaacaaactc	340
1021	ccttacaatgagtattttgagtatttcggcccagattatacgcttcatgtcgacccaagt	
1201	PYNEYFEYFGPDYTLHVDPS cctatggagaatttaaacacgcccaaagatatggagaggataaggaacacgttgctggaa	360
	PMENLNTPKDMERIRNTLLE	380
	caactttcgggactaatacacgcacctagcgtccagtttcagcacacaccaccagtcaat Q L S G L I H A P S V Q F Q H T P P V N	400
1321	cgagttttggacgagccggaagatgacatggagacaagaccaaaacctcgcatctggagt RVLDEPEDDMETRPKPRIWS	420
1381	ggaactgcgacttatgaatcagacagtgacgatgatgataaacctcttcatggttactca G T A T Y E S D S D D D K P L H G Y S	440
1441	tgtcgtggtggcgcaactacggacagggactctaccggtgaagatgaaatggatgacgat C R G G A T T D R D S T G E D E M D D	460
1501	aacccagagccagacgtgaatcctccatcgtcttaaaccagcttgatggtttggtgtctc	471
1561	N P E P D V N P P S S * ttttgccatatgataatgtcggcagatttaagaaacaagttaggggaatgaat	3 / L
1621	tgatgtttttcagcaaccttttgaqttctqtgaaaacgctgcattgattagaacagtga	
1681	caactgactagtattttggcccaagttagaaaatcagaatatgtgaaaaaaaa	
1741		



# Figure 2A

1	-cacgogtcogtaaaaatoototototttttotoaacottgattottagocatggagttotgg	
	M E F W	4
61	gqaattgaagttaaatcaggaaagccagttacagtgactcctgaagaaggcattcttatc	
	GIEVKSGKPVTVTPEEGILI	2.4
121	cacqtttctcaggcatcgcttggagaatgtaaaaacaagaagggagagtttgtgccttta	
	H V S Q A S L G E C K N K K G E F V P L	4 4
181	catgtaaaggttgggaaccagaacttggttctgggaactctatcgactgagaacatccct	
	HVKVGNQNLVLGTLSTENIP	64
241	cagettttetgtgatttggtattegaeaaggagtttgagettteteaeacttggggaaaa	
	Q L F C D L V F D K E F E L S H T W G K	84
301	ggaagtgtttactttgttggatacaaaactcccaacattgagccacaaggctattctgag	
	G S V Y F V G Y K T P N I E P Q G Y S E	
361	gaaqaagaggaagaagaagattcctqctqggaatqctqccaaggctgtagctaaa	
	E E E E E E E V P A G N A A K A V A K	124
421	ccaaaggctaagcctgcagaagtgaagccagctgttgatgatgaagaggatgagtctgat	
	P K A K P A E V K P A V D D E E D E S D	144
481	totgaoggaatggatgaagatgattotgatggtgaggattotgaggaagaagagootaca	164
	3 0 9 11 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
541	cctaagaagcctgcatcaagcaagaagagagctaatgaaactacccctaaagcacctgtg	ı 184
	PKKPASSKKRANETTPKAPV	
601	tcagcaaagaaggcgaaagtagcagttactcctcagaaaacagatgagaagaagaaaggg SAKKAKVAVTPQKTDEKKKG	204
1		
661	ggaaaggetgeaaaceagageeeaagteggeeagteaagteteatgtggtteatgeaag GKAANQSPKSASQVSCGSCK	224
701	- G K A A N Q S P K S A S Q V S C G S C K - aaqactttcaact.cagggaatgcacttgagtctcacaacaaggccaagccacgctgctgcc	
721	K T F N S G N A L E S H N K A K H A A A	
781	aaqtqaaqtggtttcttattaqagcttgtgatttctatggaattttgcctgtagtcttta	
701	- Aagrigaagriggseleleareagagelegegaeeeearggaaeeerigeoogeageooee	245
841	tgaaaccttcggattttcttatattttcttttgataacaagagtcttaatgaaagagagc	
OAI	cagttggagtcttaaaaaaaaaaaaaaagggcggccgc	
	Cayceyayeeccaaaaaaaaaaaaaaaayyyoyyeeyo	



# Figure 2B

1	gtat																				
61	atgo	gag	tta	tigg	gga	gt.t.	gag	gtic	jaca	CCa	aaa	aac	gct	a⊈t	aag	gtg	act	cat	gaa	gaa	
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121	gada	agc	att.	gtc	cac	att	tat	cag	ggat	tca	ctt	gac	tgc	aca	gtg	aaa	tat	gga	gaa	tat	
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181	gto	agt.	titt	gaġ	tgt	gac	tgt	tigo	gtgg	igge	taa	act	tgt.	tat	tgg	aac	act	ttc	aca	agac	3
	v	V	L	์ร์	V	Т	V			Α				I		Τ	$\mathbf{L}$	S	Q	D	60
241	aagt	ata	cct	caq	att	ago	ttt	gat	ittg	gtt	ttt	gat	aaa	gag	ttt	gag	ctt	tca	cac	agc	
	ĸ	F	Þ	Q	I	Ŝ	F		L			D	K	Ε	F,	Ε	L	S	Н	S	80
301	ggta	acc	aaa	gca	aat	gtt	cat	.tt.c	catt	ggc	tac	aaa	tac	aaa	aac	atc	gag	cag	gat	gac	
	Ğ	Τ	K	Ā	Ν	V	Н	F.			Y		S	Р	N	I	Ε	Q	D	D	100
361	ttca	act	agt	tag	gat	gat	gac	gat	gtt	cct	gaa	igat	gt.t.	cct	gat	cct	gcc	cct	act	gct	
	F	Т	S	S	D	D	E	D	V	Р	E	Α	V	P	А	Р	Α	Р	T	Α	120
421	gtta	act	gcc	aac	gga	aat	gat	gga	agca	igct	gtt	gtic	aag	gct	gac	aca	aag	сса	aag	gcc	
	V	T	Α	Ν	G	N	Α	G	Α	Α	V	V	K	A	D	T	K	Р	K	A	140
481	aaacctgccgaagtgaagcctgcagaagagaagcctgaatcagacgaggaagatgagtct																				
	K								E					S			E		E	<u>S</u>	160
541	ga:	tga	t.ga	aga	tga	igto	tga	aga	agga	itga	itga	ecto	:t:ga	gaa	agg	aat	gga	tgt	tga	t.gaa	3.
	D	D	E	D	E		_E	E_		D	D	S		K_	_			V	D_	F.	180
601	gate	gac	tca	gat	gat	gac	gaç	gag	ggaç	gat	itiqt	gaç	gat	gaa	gaa	gag	gag	gag	act	cat	
	D	D	S		D		E	Е	E	D	S			F.		Ε	E	E	Т	Ρ	200
661																					
	K	K	Р	Ε	P	Ι	И	K		R		N	F,		V		K	Т	Р	V	220
721	tct	gga	aag	aag	gca	aaa															
	S	G	K	K		K			А				S	Τ	Þ	Q	K	Т	Ε	K	240
781	aag	aaa	gga	.gga	cac	acc															0.60
	K	K	G	G	Н	T	A		P			А		K				S	E,	V	260
841	aat	gct		cag																	200
	N	А	И	Q		Р			G		_	S		G		N	N	N	K	K	280
901	cca																				200
	Б	F	Ν	_	G		Q		G				N		G	S				K	300
961	gga						gga	cgt	tgga	atca	aagg	gaga	ıggt	ttt	ggg	tt	tcg	agt	aga	tga	205
	G		G	R	А	*															305
021	tga.	aaa	cac	ttg	gaa	igte	gtgo	ghti	ttgç	gatt	ttt	ato	itta	ittt	tat	tag.	tat.	aac	ttg.	tta	
081	t.cg																				
141	tat	t.t.g	ctg	aaa	ıtga	agaa	aaga	aaga	act.c	cgaa	ait.it.c	gcaa	aaca	ıaaa	aaa	aaa	aaa	aaa	aaa	aaa	
201	aag	ggc	ggd	cgc	;																

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## Figure 3

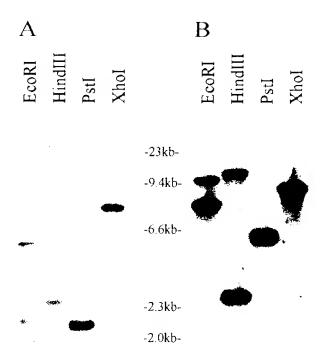
 and the second second			´			
<sup>1</sup> AtRPD3A AtRPD3B ZmRPD3 RPD3	MDTGG MEADESGI MDPSSAGSGG MVYEATPFD-	NSLAS-GPDG -SLPS-GPDG NSLPSVGPDGPITVKPS	VKRKVCYFYD PKRRVSYFYE QKRRVCYFYD DKRRVAYFYD	PEVGNYYYGQ PTIGDYYYGQ PDVGNYYYGQ ADVGNYAYGA	GHPMKPHRIR GHPMKPHRIR GHPMKPHRIR GHPMKPHRIR	44 47 50 46
AtRPD3A AtRPD3B ZmRPD3 RPD3	MTH <mark>A</mark> LLAHYG M <mark>A</mark> HSLIIHYH MTHSLLA <mark>R</mark> YG M <mark>A</mark> HSLIMNYG	LLQH <mark>MQV</mark> LKP LHRRLEISRP LLNQMQVYRP LYKKMEIYR	FPARERDLCR SLADASDIGR NPARERELCR KPATKQEMCQ	FHADDYVSEL FHSPEYVDFL FHAEEYINFL FHTDEYIDFL	RSITPETQQD ASVSPESMGD RSVTPETQQD SRVTPDNLEM	94 97 100 96
AtRPD3A AtRPD3B ZmRPD3 RPD3	QIRQLKRF PSAARNLRRF QIRLLKRF FKRESVKF	NVGEDCPVFD NVGEDCPVFD NVGE <mark>E</mark> CPVLD NVG <mark>D</mark> DCPVFD	GLYSFCQTYA GLFDFCRASA GLYSFCQTYA GLYEYCSISG	GGSVGG <mark>S</mark> VKL GGS <mark>IGA</mark> AVKI GASVGGAVKF GGS <mark>ME</mark> GAARI	NHGLCDIAIN NRQDADIAIN NHGH-DIAIN NRGKCDVAVN	142 147 147 144
AtRPD3A AtRPD3B ZmRPD3 RPD3	WAGGLHHAKK W <mark>G</mark> GGLHHAKK W <mark>S</mark> GGLHHAKK YAGGLHHAKK	CEASGFCYVN SEASGFCYVN CEASGFCYVN SEASGFCYLN	DIVLAILELL DIVLGILELL DIVLAILELL DIVLGI <mark>I</mark> ELL	KQHERVLYVD KMFKRVLYID KHHERVLYVD RYHPRVLYID *	IDIHHGDGVE IDVHHGDGVE IDIHHGDGVE IDVHHGDGVE	192 197 197 194
AtRPD3A AtRPD3B ZmRPD3 RPD3	EAFYATDRVM EAFYTTDRVM EAFYTTDRVM EAFYTTDRVM *	TVSFHKFGDY TVSFHKFGDF TVSFHKFGDY TCSFHKYGEF * *	FPGTGHIQDI FPGTGHIRDV FPGTGDIRDI FPGTGELRDI	GA <mark>G</mark> AGK <mark>N</mark> AA GHSKGKAAST GAE	NVPLDDGIDD NVPL <mark>NDGM</mark> DD NVPLDDGIDD NVPL <mark>R</mark> DGIDD	242 247 247 244
AtRPD3A AtRPD3B ZmRPD3 RPD3	ESYHLLFKPI ESFRSLFRPL ESYQSLFKPI ATYRSVFEPV	MGKVME <mark>I</mark> FRP I <mark>Q</mark> KVMEVYQP MGKVMEVFRP IKKIME <mark>W</mark> YQP	GAVVLQCGAD <mark>E</mark> AVVLQCGAD GAVVLQCGAD SAVVLQCG <mark>G</mark> D	SLSGDRLGCF SLSGDRLGCF SLSGDRLGCF SLSGDRLGCF	NLSIKGHAEC NLS <mark>V</mark> KGHA <mark>D</mark> C NLSIKGHAEC NLS <mark>ME</mark> GHA <mark>N</mark> C	292 297 297 294
AtRPD3A AtRPD3B ZmRPD3 RPD3	VKFMRSFNVP LRFLRSYNVP VRYMRSFNVP VNYVKSFGIP	LLLLGGGGYT LMVLGG <mark>E</mark> GYT LLLLGGGGYT MMVVGGGGYT	IRNVARCWCY IRNVARCWCY IRNVARCWCY MRNVARTWCF	ETGVALGVEV ET <mark>AVAV</mark> GVEP ETGVALG <mark>Q</mark> EP ETGLLNNVVL	DKDTЬÄNEÄÄ EDKWBANEÄÄ EDKWBEHEÄÄ	342 347 347 344
AtRPD3A AtRPD3B ZmRPD3 RPD3		VD <mark>PSNMENKN</mark> VAPSNMENKN	TPKDMERIRN TROOLDDIRS	DLLHNLSKLQ TLLHNLSGLI KLSKLR NIFANLENTK	HAPSVQFQHT HAPSV <mark>H</mark> FQER	392 397 393 394
AtRPD3A AtRPD3B ZmRPD3 RPD3	PPVNRVLD	EDQDDPDERH	EPEDDME DPDSDMEVDD	DR TR HKAVEESSRR DSA	KPRIWSG SILG <mark>I</mark> KIKRE	434 421 443 409
AtRPD3A AtRPD3B ZmRPD3 RPD3	AVEPDTKDKD TATYESDSDD FGENATRVQD	GLKGIMERGK DDKPLHGY GGRVASEH-R	GCEVEVDESG SC GLEPMAEDIG	STKVTGV RGGATTDR SSKQAPQADA	NPVGVEEAS- DSTGEDEMDD SAMAIDEPSN EAKD	480 459 492 413
AtRPD3A AtRPD3B ZmRPD3 RPD3	VKMEEEGTNK DNPEPDVNP- VKNEPESSTK TKGGSQYARD	PSS Logqaaayhk	T P			501 471 513 433



# Figure 4

AtHD2A AtHD2B ZmHD2	MEFWGIEVE <mark>S MEFWGVAVT</mark> E MEFWGLEVEF	SKPVTVTPEE KNATEVTPEF GSTVFCEFGY	GILIUVSÕAS DSIVHISÕAS GFVLHLSÕAA	LGECKNEEGE J-DOTVESGE LGESKESD	FVPLHVKVGN SVVLSVTVGG NALMYVKIDD	50 49 48
AtHD2A AtHD2B ZmHD2	QNLVLSTLST AKLVIGTUSQ QKLAISTUSV	ENIPOLFODI DEPPOISEDL DENPHIQEDI	VFDKEFELSH VFDKEFELSH IFDKEFELSH	TWGKGSVYFV SGTFANVHFI TSKTTSVFFT	GYKTPNIE PQ GYKSPNIE QD GYKVE QPFEE	100 99 98
AtHD2A AtHD2B 2mHD2	GYSEEEEEE- DFTSSDDECV DEMDLDSEDE	EEEVPAGNAA PEAVPAPAPT DEELNVP	AVTANGNAGA VVKENGKADE	KAVARPE AVVKADTRPE KKQESQEKAV	ÄKPAEVKPAV AKPAEVKPAE A <mark>A</mark> PSKSSPDS	136 149 145
AtHD2A AtHD2B ZmHD2	D <mark>DEEDE</mark> K <mark>K</mark> SKDDDDSD	SDS-D SDDEDESEED EDETDDSDED	GMD DDSEKSMD ETDDSDESLS	EDDSDGEDSE VDEDDSDDDF SEEGDDDSSD	EEEEEEEEEEEEEEEEEE	162 197 195
AtHD2A AtHD2B ZmHD2	PTPKKPAS ETPKKPEP DTPTPKKPKV	-SKKRANLTT INKKRPNESV GKKRP <mark>A</mark> ES <mark>S</mark> V	PK <mark>APVŠA</mark> KA SKTPVSGKKA LKTPLSDKKA	KVAVTP KPAAAPASTP KVATPSS	OKTDEKK OKTGGK	202 240 238
AthD2A AthD2B ZmHD2	-KGGKA KKGGHTAT -KGAAVHVAT	PHPAK PHPAKGKTIV	AN KGG <mark>KS</mark> PVNAN NND <mark>KS</mark> VKSPK	QSPKS <mark>AS</mark> QVS QSPKSGGQ <mark>S</mark> S SA <mark>PKSGG</mark> SVP	COSO-KKTEN GONNNKKPEN CKPOSK-SF1	229 283 286
AtHD2A AtHD2B ZmHD2	SGNALE-SHN SGKQFGGSNN SETALQA-HS	KAK <mark>HAAA</mark> K KGSNKGKGKG R <mark>AK</mark> MGASESQ	RA VQ			245 305 307





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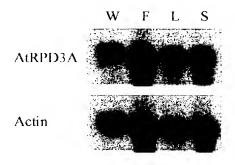
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-2.0kb-







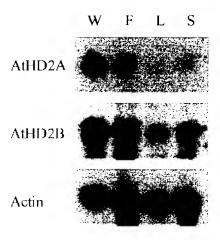




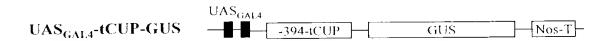
Figure 9

A

#### **Effector Plasmids**



#### **Reporter Plasmid**



В

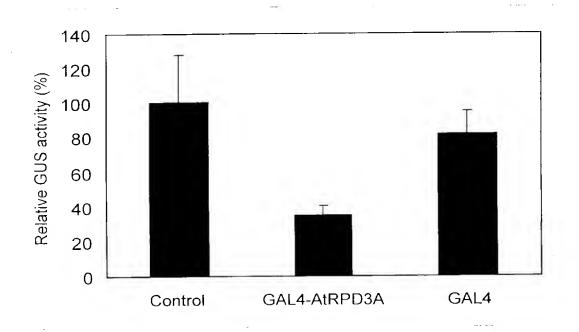
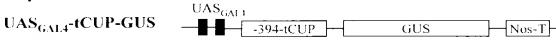
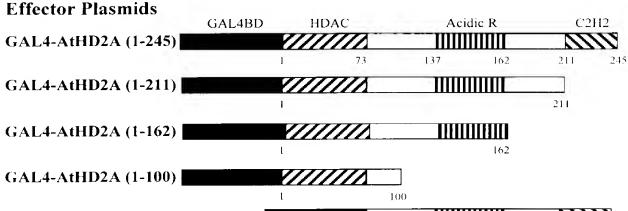


Figure 10







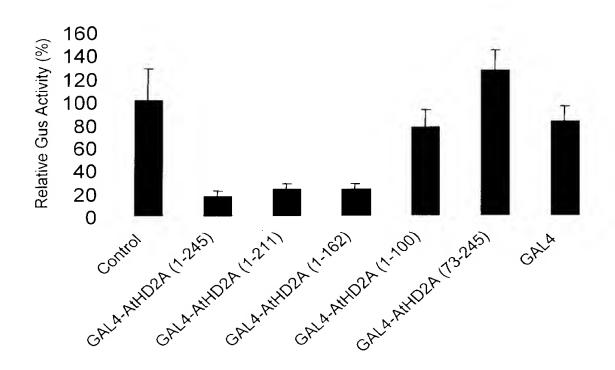
73

245

**GAL4** 

GAL4-AtHD2A (73-245)

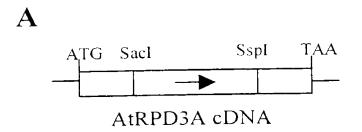
B

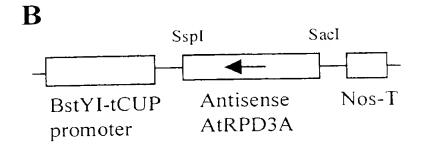


RECEIVED

SEP 1 2 207

TECH CENTER 1600.2900







	₩ F B2	BS A1	
Endogenous AtRPD3A	-		1.6kb
Antisense AtRPD3A			- 0 6 <b>kb</b>
Actin	90	99	1.5kb

SEP 0 9 MMZ SEE

#### FIGURE 13

WT 1 2 3 4 5

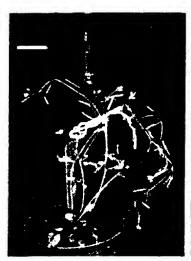
Endogenous AtHD2A

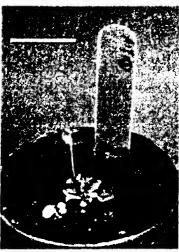


Antisense AtHD2A









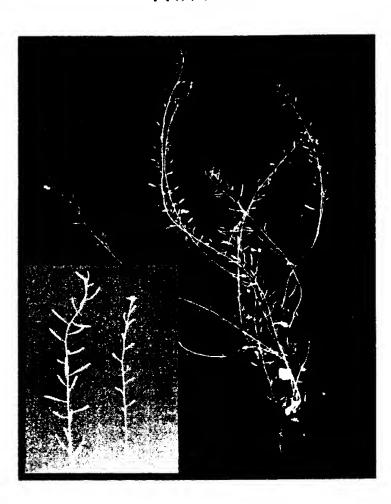




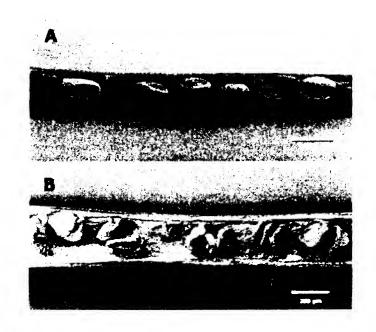
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TECH CENTER 1600/2900

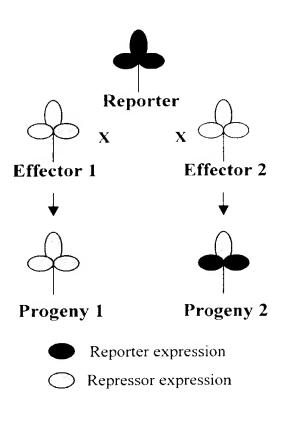








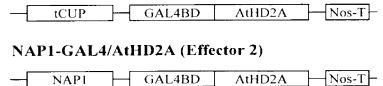
A



B

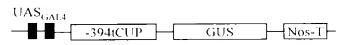
#### **Effector Plasmids**

#### tCUP-GAL4/AtHD2A (Effector 1)



#### Reporter Plasmid

#### $UAS_{GAL4}\hbox{-}tCUP\hbox{-}GUS \ (or\ UAS_{GAL4}\hbox{-}35S\hbox{-}GUS)$



# Figure 17



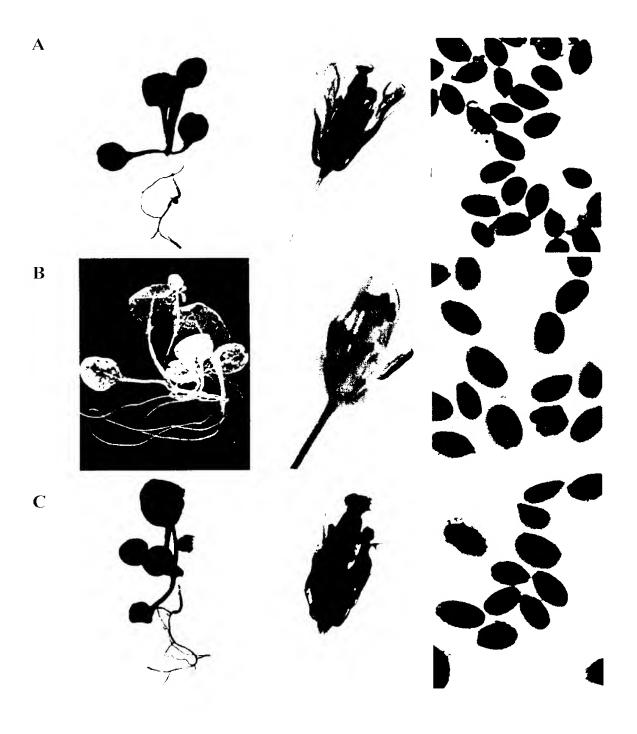


Figure 18



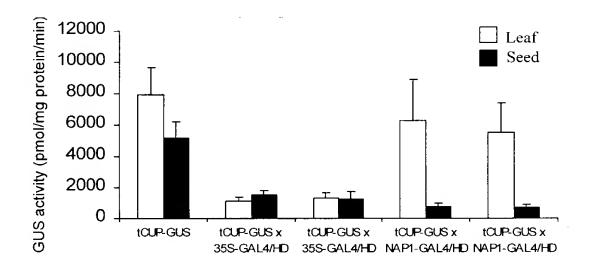


Figure 19A

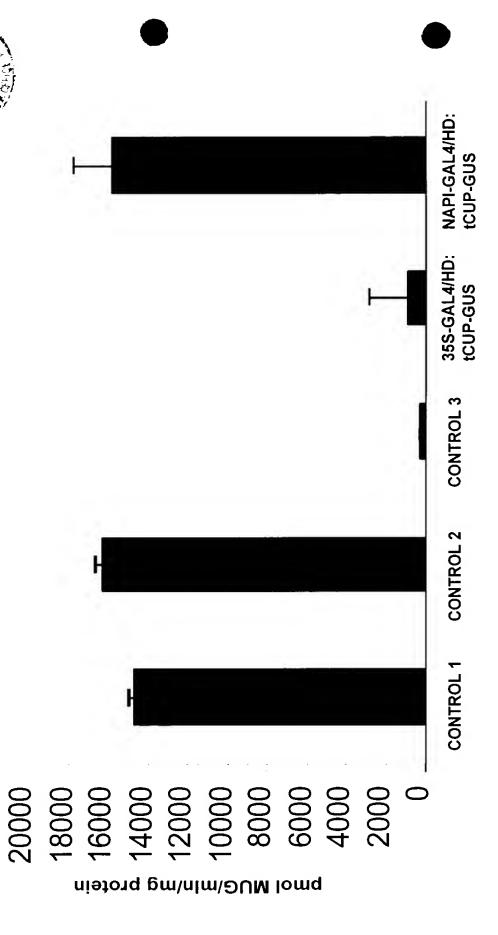


Figure 19B

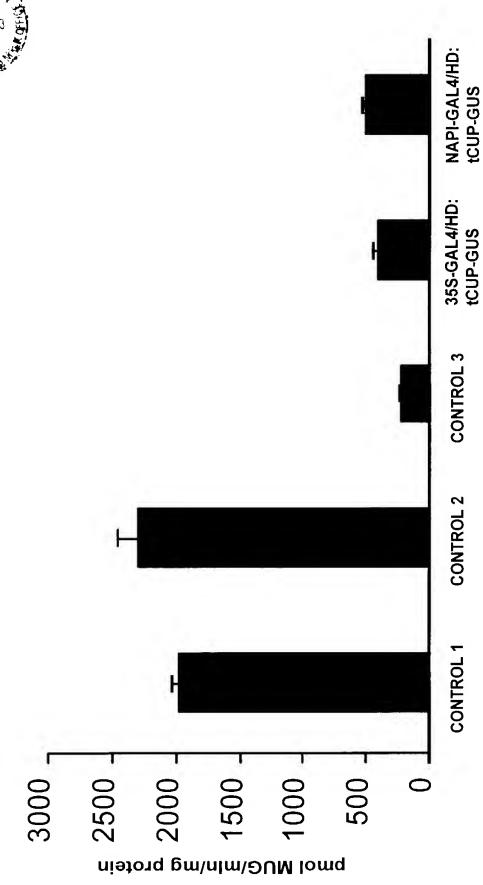


Figure 19C

APR 2 1 2003

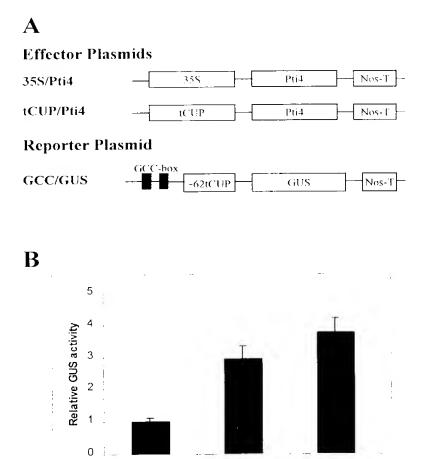


Figure 20

35S/Pti4

Control

tCUP/Pti4



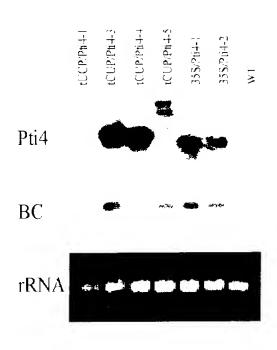


Figure 21



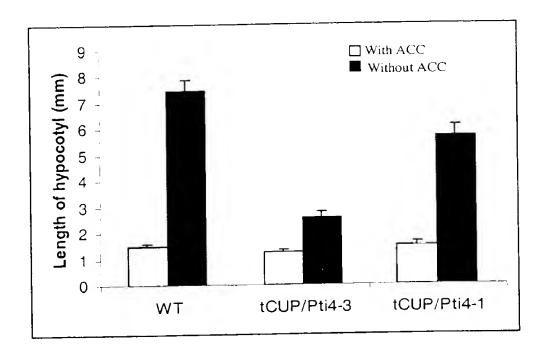


Figure 22



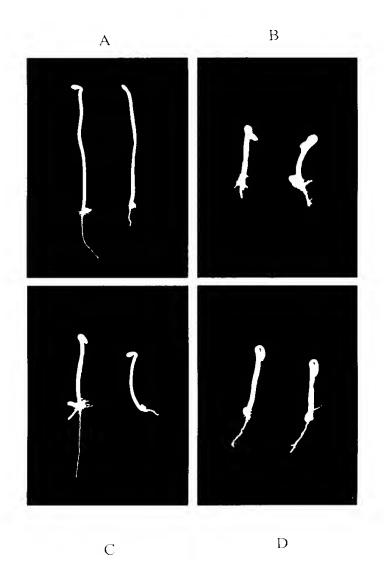


Figure 23



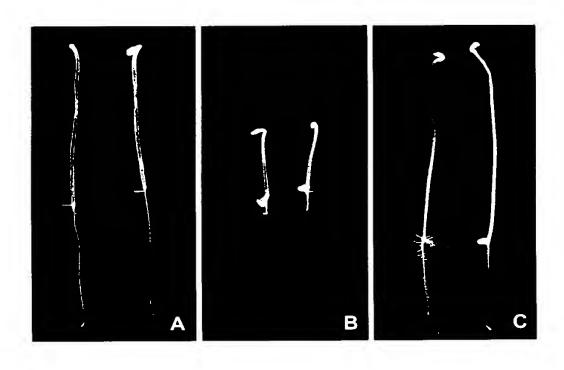


Figure 24